Phyre2

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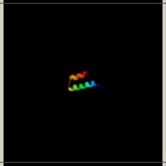
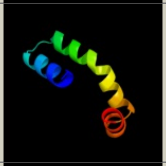
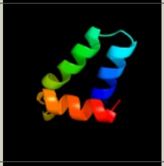
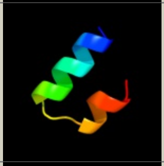
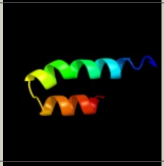
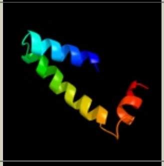
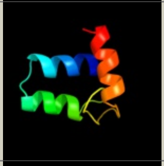
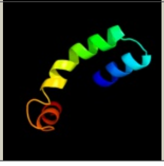
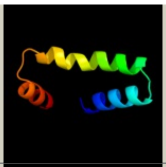
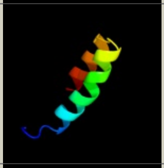
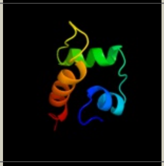
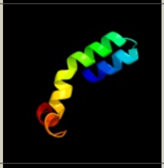
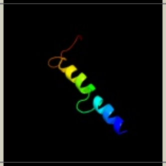
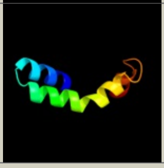
Unique Job ID	8098413ed7cca2d9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3f40A_	Alignment		23.0	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized ntf2-like protein; **PDBTitle:** crystal structure of ntf2-like protein of unknown function2 (yp_677363.1) from cytophaga hutchinsonii atcc 33406 at3 1.27 a resolution
2	d1sr2a_	Alignment		19.7	3	**Fold:**Four-helical up-and-down bundle **Superfamily:**Histidine-containing phosphotransfer domain, HPT domain **Family:**Sensor-like histidine kinase YojN, C-terminal domain
3	c3na8A_	Alignment		15.8	4	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
4	d1iqpa1	Alignment		15.6	11	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**DNA polymerase III clamp loader subunits, C-terminal domain
5	c3ff2A_	Alignment		14.7	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized cystatin fold protein (yp_497570.1) from **PDBTitle:** crystal structure of an uncharacterized cystatin fold protein2 (saro_2299) from novosphingobium aromaticivorans dsm at 1.90 a3 resolution
6	d1wn0a1	Alignment		14.1	12	**Fold:**Four-helical up-and-down bundle **Superfamily:**Histidine-containing phosphotransfer domain, HPT domain **Family:**Phosphorelay protein-like
7	c3h5dD_	Alignment		13.2	13	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** dihydrodipicolinate synthase from drug-resistant streptococcus2 pneumoniae
8	d256ba_	Alignment		13.2	16	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome b562
9	c3soyA_	Alignment		12.8	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**ntf2-like superfamily protein; **PDBTitle:** nuclear transport factor 2 (ntf2-like) superfamily protein from2 salmonella enterica subsp. enterica serovar typhimurium str. lt2
10	d1sxjc1	Alignment		12.4	11	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**DNA polymerase III clamp loader subunits, C-terminal domain
11	c3si9B_	Alignment		12.1	7	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from bartonella2 henselae

12	c3eb2A_	Alignment		11.9	6	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution
13	c3op1A_	Alignment		11.4	5	**PDB header:**transferase **Chain:** A: **PDB Molecule:**macrolide-efflux protein; **PDBTitle:** crystal structure of macrolide-efflux protein sp_1110 from2 streptococcus pneumoniae
14	d1yvia1	Alignment		11.4	12	**Fold:**Four-helical up-and-down bundle **Superfamily:**Histidine-containing phosphotransfer domain, HPT domain **Family:**Phosphorelay protein-like
15	c2x0kB_	Alignment		11.0	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin biosynthesis protein ribf; **PDBTitle:** crystal structure of modular fad synthetase from2 corynebacterium ammoniagenes
16	d2gqba1	Alignment		10.9	9	**Fold:**RPA2825-like **Superfamily:**RPA2825-like **Family:**RPA2825-like
17	c1t6zB_	Alignment		10.8	0	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin kinase/fmn adenylyltransferase; **PDBTitle:** crystal structure of riboflavin bound tm379
18	d1o5ka_	Alignment		10.7	4	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
19	c3ixzB_	Alignment		10.6	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**potassium-transporting atpase subunit beta; **PDBTitle:** pig gastric h+/k+-atpase complexed with aluminium fluoride
20	c3bi8A_	Alignment		10.5	4	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of dihydrodipicolinate synthase from clostridium2 botulinum
21	d2a6na1	Alignment	not modelled	10.5	6	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
22	c3noeA_	Alignment	not modelled	10.1	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
23	d1xkya1	Alignment	not modelled	9.7	4	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
24	c3ehcA_	Alignment	not modelled	9.4	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**snoal-like polyketide cyclase; **PDBTitle:** crystal structure of a snoal-like polyketide cyclase (atu3018) from2 agrobacterium tumefaciens str. c58 at 2.12 a resolution
25	c2vc6A_	Alignment	not modelled	9.0	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of mosa from s. meliloti with pyruvate bound
26	c3myfB_	Alignment	not modelled	9.0	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sensor protein; **PDBTitle:** the crystal structure of the hpt domain from the hpt sensor hybrid2 histidine kinase from shewanella to 1.80a
27	c2ehhE_	Alignment	not modelled	8.8	11	**PDB header:**lyase **Chain:** E: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
28	c3fluD_	Alignment	not modelled	8.7	11	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis

29	d2k54a1	Alignment	not modelled	8.5	21	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Atu0742-like
30	c3b8eB_	Alignment	not modelled	8.2	14	**PDB header:**hydrolase/transport protein **Chain:** B: **PDB Molecule:**sodium/potassium-transporting atpase subunit **PDBTitle:** crystal structure of the sodium-potassium pump
31	d1hynp_	Alignment	not modelled	8.2	23	**Fold:**Phoshotransferase/anion transport protein **Superfamily:**Phoshotransferase/anion transport protein **Family:**Anion transport protein, cytoplasmic domain
32	c1hynQ_	Alignment	not modelled	8.1	23	**PDB header:**membrane protein **Chain:** Q: **PDB Molecule:**band 3 anion transport protein; **PDBTitle:** crystal structure of the cytoplasmic domain of human2 erythrocyte band-3 protein
33	c3f8hA_	Alignment	not modelled	7.4	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative polyketide cyclase; **PDBTitle:** crystal structure of a putative polyketide cyclase (tm1040_3560) from2 silicibacter sp. tm1040 at 2.00 a resolution
34	d1hw1a2	Alignment	not modelled	7.4	13	**Fold:**GntR ligand-binding domain-like **Superfamily:**GntR ligand-binding domain-like **Family:**GntR ligand-binding domain-like
35	c3g0sA_	Alignment	not modelled	7.3	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** dihydrodipicolinate synthase from salmonella typhimurium lt2
36	d2gxfa1	Alignment	not modelled	6.9	14	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**YybH-like
37	c3pueA_	Alignment	not modelled	6.9	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of the complex of dhydrodipicolinate synthase from2 acinetobacter baumannii with lysine at 2.6a resolution
38	c3s5oA_	Alignment	not modelled	6.3	4	**PDB header:**lyase **Chain:** A: **PDB Molecule:**4-hydroxy-2-oxoglutarate aldolase, mitochondrial; **PDBTitle:** crystal structure of human 4-hydroxy-2-oxoglutarate aldolase bound to2 pyruvate
39	c3mv2A_	Alignment	not modelled	6.1	19	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**coatomer subunit alpha; **PDBTitle:** crystal structure of a-cop in complex with e-cop
40	c3lerA_	Alignment	not modelled	5.5	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
41	d1y6da_	Alignment	not modelled	5.4	5	**Fold:**Four-helical up-and-down bundle **Superfamily:**Histidine-containing phosphotransfer domain, HPT domain **Family:**Phosphorelay protein luxU
42	c3k1sE_	Alignment	not modelled	5.3	14	**PDB header:**transferase **Chain:** E: **PDB Molecule:**pts system, cellobiose-specific iia component; **PDBTitle:** crystal structure of the pts cellobiose specific enzyme iia2 from bacillus anthracis
43	c2ksnA_	Alignment	not modelled	5.2	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ubiquitin domain-containing protein 2; **PDBTitle:** solution structure of the n-terminal domain of dc-ubp/ubtd2
44	c2pcqA_	Alignment	not modelled	5.2	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthase; **PDBTitle:** crystal structure of putative dihydrodipicolinate synthase (ttha0737)2 from thermus thermophilus hb8
45	d3dmca1	Alignment	not modelled	5.1	0	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**PhzA/PhzB-like
46	c3sn6R_	Alignment	not modelled	5.1	6	**PDB header:**signaling protein/hydrolase **Chain:** R: **PDB Molecule:**lysozyme, beta-2 adrenergic receptor; **PDBTitle:** crystal structure of the beta2 adrenergic receptor-gs protein complex